

## EXHIBIT 2

```

#####
# Program: needle
# Rundate: Mon Jul 31 06:58:16 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060731-06581567407497.output
#####

#=====
#
# Aligned_sequences: 2
# 1: SEQ175
# 2: G_kausotphilus
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 553
# Identity: 252/553 (45.6%)
# Similarity: 252/553 (45.6%)
# Gaps: 119/553 (21.5%)
# Score: 1104.5
#
#
#=====

SEQ175      1      atgattaaccgcgtc---attttggtcggcagg-----ttaa      34
      ..|...|...|...|  |||  |||...|...|...|...|  ||..
G_kausotphilu  1  ttaaaacggcaaatcatcatcagaaatatcgatcggtcgccgctcattgg      50

SEQ175      35  cgaga-gatc-----cggagttgcgttacac---tccaagcggga-----g      70
      |||...|...|  |||  |||...|...|...|...|  |||...|...|  |
G_kausotphilu  51  cgaaaggatcgtcacatcgatcgcgccaaaccctttttcgttcggatattgg      100

SEQ175      71  tgg--ctg---ttgccacgtttacg-----ctcgcggtcaaccgctc-      106
      |||  |||  |||  |||...|...|  |||...|...|  |||...|...|
G_kausotphilu  101 tggttctgatcttgcc-cgaatgggaatggatccccatagt-agccgcct      148

SEQ175      107 -cgtttacaaatcagcaggcgagcggg--aaacggattttattcaatgt      153
      |...|...|...|  |||...|...|...|...|  |||...|...|  |...|...|
G_kausotphilu  149 gctgttgccctc-gctgctcgctcgttcctttcggc--tcaagaaattg      195

SEQ175      154 gtcgtttggcgccgcca-----ggcg-gaaaacgtcgccaactttttgaa      197
      |...|...|...|...|  |||  |||...|...|...|...|  |||...|...|
G_kausotphilu  196 gacgctatcagccaccacttccgtcacgtacag-cgccgaccttcttga      244

SEQ175      198 aaaggggagcttggttg--tgtcgatggccgactgcaaaccgc--agc      243
      .....|...|...|  |||  |||...|...|...|...|  |||...|...|
G_kausotphilu  245 ttttcatagt--gcgggtttgcagtcggccatcgac--accagccaagc      290

SEQ175      244 tatgaaaatcaagaaggtcggtg-gtgtacgtgacggaagtgggtgctg      292
      |.....|...|...|...|...|  |||...|...|  |||...|...|
G_kausotphilu  291 tcccccttttcaaaaagttggcgacgttttc-cgcc-----tggcggcgc      334

SEQ175      293 atagcgtccaattttcttgag--ccgaaaggaacgagcgagcagcagggg      340
      ..|...|...|...|...|  |||...|...|...|...|  |||...|...|
G_kausotphilu  335 caaacgacacattgaataaaatcgttt--cccgctcgccctgc-tgatt      381

SEQ175      341 cgacagcaggcggct-actatggggatccattcccatcgggcaagatca      389
      |...|...|...|...|  |||...|...|  |||...|...|  |||...|...|
G_kausotphilu  382 tgtaaacggacggttgaccgcgag---cgtaaacgt---ggcaa---ca      421

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SEQ175      390 gaaccaccaatatccgaacgaaaaaggggttgccgcgcgcgatgaacgac 439
      |  ||||  ||||...|  ||||  |||||  ||||...
G_kausotphilu 422 g--ccac-----tccgcttg----gagtgt-aacgcaac---tccggat 455
SEQ175      440 ctttcgccaatgacggccagccgatcgatattttgatgatgatgttgcgc 489
      ||.||||.||  ||.|||||.||.|||||  ||.||||  |.
G_kausotphilu 456 ctctcggttaa-----cctgccgaccacaaatgac-gcgggttaat----ca 494
SEQ175      490 ttt      492
      |
G_kausotphilu 495 t      495

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SEQ175      405 gaacgaaaaagggtttggccgcgcgatgacgatccctttgccaatgacg      454
      .||||.|||||      |.|||.|||      ||| |.|||.|||.|||.|||
B_cereus    421 taacgtaaaag---tagctactgc---gac-accattggcggtgtaacg      462
      .||||.||||.||||      |.|||.|||      |.|||.|||.|||.|||
SEQ175      455 ---gccagccgatcgatat---ctgatgatgatttgccggtt      492
      |.|||| |.||||.|||      |.|||.|||.|||.|||.|||
B_cereus    463 taagtcag--ggtccttagttaaacgaccaacgaggataaacacgattcat      510
      .||||.||||.||||      |.|||.|||.|||.|||.|||
SEQ175      493      492
B_cereus    511 caa      513

```

```
#####
# Program: needle
# Runday: Mon Jul 31 07:14:27 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060731-07142621848170.output
#####
```

```
#####
#
# Aligned_sequences: 2
# 1: SEQ175
# 2: B_anthraxis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 577
# Identity: 237/577 (41.1%)
# Similarity: 237/577 (41.1%)
# Gaps: 131/577 (22.7%)
# Score: 1040.5
#
#=====
```

SEQ175	1	atgattaaccg-cgtcattttggtcggcagggttaacgagagatcc	44
B_anthraxis	1	ttagaacggtaaatcgtcgtcggaatgtcgatcggttgac-ctacattt	49
SEQ175	45	ggagttg---cggtacactcc---aagcggagtggt---gttgccacg	84
B_anthraxis	50	gaaaatggatcgtcattcttcgtaaatccagagtttccttggttaccttg	99
SEQ175	85	tttacgc-----tcgcgggtcaacc-----gtcc---gtttacaa	115
B_anthraxis	100	gttgcccggaattactagattgaccaaagggttagagctttggttacoga	149
SEQ175	116	atcagcagggcgagcgggaacggattttattcaatgtgtcgtttgccgc	165
B_anthraxis	150	aac--cagctcctgatggttggtgattaaatgaaccaagttgctcccccac	197
SEQ175	166	cgcca-----ggcggaaaacgtcgccaactttttgaaaaagggagctt	209
B_anthraxis	198	cgccattacgcggctctaaaaattgtacgctttccgcaa----gaactt	242
SEQ175	210	ggctggtgtcgatggccgactgcaaaccgcagctatgaaaatcaagaag	259
B_anthraxis	243	--ctgttacatatacacgcttaaccatcttgcctcgttaattacgagttt	290
SEQ175	260	gtcggcgtgtgtacgtgacggaagtgttggt---gatagcg	298
B_anthraxis	291	gaagacgtccatctacgcctgctaagctaccttttttaataatttgc-	339
SEQ175	299	tccaatttc-----ttgagccgaaagggaacgagcga----gcagcga	336
B_anthraxis	340	tacgttttctgctgtttacgcatattacacaattaataaagtcagctt	389
SEQ175	337	ggggcgacagcagggcgtactatggggatccattccca---ttcgggca	383
B_anthraxis	390	cacgc-tcaccttggtgattcgcaaatgcgcgattcacagctaactgaaa	438

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SEQ175      384 ag---atcagaaccaccaatatccg---aacgaaa--aagggt----- 418
      ||      ..|.|.|.|||||.||...||  ||||.||  .|||||
B_anthraxis 439 agtagctactgcaacaccattggggcgtgtaacgtaagtcagggtccttag 488
SEQ175      419 ttggccg--catcgatgacgatcc-tttcgccaatgacggccagccgatac 465
      ||...||  |||||||.||..||..  .||||.||||  ||..|.
B_anthraxis 489 ttaaacgaccaacgaggataaacacgattcatcaat--cgaaccac 531
SEQ175      466 gatatttctgatgatgatttgccgttt 492
B_anthraxis 532
      531

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```
#####
# Program: needle
# Rundate: Mon Jul 31 07:15:58 2006
# Align_format: srepair
# Report_file: /ebi/extraerv/old-work/needle-20060731-07155589573420.output
#####
```

```
#=====
#
# Aligned_sequences: 2
# 1: SEQ175
# 2: B_thuringiensis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 556
# Identity: 238/556 (42.8%)
# Similarity: 238/556 (42.8%)
# Gaps: 98/556 (17.6%)
# Score: 1029.5
#
#=====
```

SEQ175	1	atgattaacgc-cgtcatttttggtcggcagggttaacgagagatcc	44
B_thuringiens	1	ttagaacggtaaatcgtcgtcggaatgtcgatcggttgac-ctacattt	49
SEQ175	45	ggagttg---cgttacactcc---aagcggagtggt---gttgccacg	84
B_thuringiens	50	gaaaatggatcgtcattcttcgtaaaatccagagtttcttggttaccttg	99
SEQ175	85	tttacgc-----tcggcgtaacc-----gtcc---gtttacaa	115
B_thuringiens	100	gttgcccgaaattactagattgaccaaattgggttagagctttggttacga	149
SEQ175	116	atcagcagggcgagcgggaaacggattttattcaatgtgtcgtttggcgc	165
B_thuringiens	150	aac--cagctcctgatggttgctgattaaatgaaccagttgctcccccac	197
SEQ175	166	cgcca-----ggcggaacgcgcgaactttttgaaaaagggagctt	209
B_thuringiens	198	cgccattacgcggctctaaaaattgtacgctttccgcaa----gaactt	242
SEQ175	210	ggctggtgtcgatggccgactgcaaaccgcagctatgaaaatcaagaag	259
B_thuringiens	243	--ctgttacatatacacgcttaccatcttgcctcgttaattacgagttt	290
SEQ175	260	gtcggcgtgtgtacgtgacggaagtgttggtgatagcgtccaatttctt	309
B_thuringiens	291	gaagacgtccatctacgcctgctaagctaccttttt---tcaaataattt	337
SEQ175	310	gagccgaaagggaacgagcagcagcagggcgaca-----gcaggcgg	353
B_thuringiens	338	gtacggtttctgctgtttacgccatattac-acaattaataaagtcag	386
SEQ175	354	ctactatggggatccattccattcgggcaagatcagaaccaaccaatc	403
B_thuringiens	387	cttcac--gtcaccttggtgattcg-----caaatgcgcgattcac	426









```
#####
# Program: needle
# Rundate: Mon Jul 31 07:19:15 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060731-07191488315985.output
#####

#=====
#
# Aligned_sequences: 2
# 1: SEQ175
# 2: B_subtilis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 528
# Identity: 350/528 (66.3%)
# Similarity: 350/528 (66.3%)
# Gaps: 45/528 ( 8.5%)
# Score: 1860.0
#
#=====

SEQ175      1 atgattaaccgcgctcattttggcgccagggttaacgagagatccggagtt 50
              |||..|||||..||..||..||..||..||..||..||..||..||
B_subtilis  1 atgcttaaccgagttgtattagtcggaagactgacaaaagaccagagct 50

SEQ175      51 gcgttacactccaagcggagtggtgtgcccagtttacgctcgcggtca 100
              .||||..||..||..||..||..||..||..||..||..||..||
B_subtilis  51 tcgttatacgccaaacggtgcggctgttgctacgtttactcttgctgtga 100

SEQ175      101 accgtccggtttacaaatcagcagggcgagcgggaaacggattttattcaa 150
              |..||..||..||..||..||..||..||..||..||..||..||..
B_subtilis  101 atcgtaacatttacgaaccagtcgggagaacgtgagggcgatttcattaat 150

SEQ175      151 tgtgtcggtttggcgccgcagggcggaacgtcgccaactttttgaaaaa 200
              |||||..||..||..||..||..||..||..||..||..||..||..
B_subtilis  151 tgtgtcacttgagagaagacagccgaaacgttgcaaaccttcttgaaaaa 200

SEQ175      201 ggggagcttggtgtgtgtcgatggcgactgcaaaccgcagctatgaaa 250
              .||..||..||..||..||..||..||..||..||..||..||..
B_subtilis  201 aggaagccttgaggcgtagatggccgtttacaaacaagaaactatgaaa 250

SEQ175      251 atcaagaaggtcgcggtgtgtacgtgacggaagtgggtggtgatagcgtc 300
              |..||..||..||..||..||..||..||..||..||..||..||..
B_subtilis  251 accagcaaggacagcggtgtcttcgtgacagaggtccaagctgaaagtgtt 300

SEQ175      301 caatttcttgagccgaaaaggaacg--agcg-----ag-----c 331
              |||||..||..||..||..||..||..||..||..||..||..||..
B_subtilis  301 caatttcttgagccgaaa--aacggcgggcggttctggttcaggtggatac 348

SEQ175      332 agcgaggg--gcgacagcaggggc---tactatgg-gga-tccattc-- 372
              |..||..||..||..||..||..||..||..||..||..||..||..
B_subtilis  349 aacgaaggaaacagcggc-ggagggccagtactttggcggaggccaaaatg 397

SEQ175      373 -----ccattcgggcaagatcagaaccaccaatatccgaacgaaaaaggg 417
              |||||..||..||..||..||..||..||..||..||..||..||..
B_subtilis  398 ataatccatttgggggaaatcaaaacaaccagagac---gcaatcagggg 444
```

```

SEQ175          418 tttggcgcgatcgatgacgatcctttcgccaatgacggccagccgatcga      467
                  ..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|
B_subtilis      445 --aacagctttaatgatgacccatttgccaacgacggccaaacgattga      491

SEQ175          468 tattctcgatgatgatttgcgcttt      492
                  .|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|
B_subtilis      492 catctcggatgatgatcttccattctaa      519

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```
#####
# Program: needle
# Rundate: Mon Jul 31 07:20:15 2005
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060731-07201389109922.output
#####

#=====
#
# Aligned_sequences: 2
# 1: SEQ175
# 2: B_licheniformis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 566
# Identity: 253/566 (44.7%)
# Similarity: 253/566 (44.7%)
# Gaps: 127/566 (22.4%)
# Score: 1124.0
#
#=====

SEQ175      1      atgattaaccg-cgtc---attttggtcggcaggttaacgagag      40
              |||...|...| |...| |...|...|...| |...|
B_licheniform 1 ttaaaatggcaagtgcgtcatcagagatgtcaatcggc---tttcc----      42

SEQ175      41 atccggagttgcgttacactccaagcggagtggtgttgccacgtttacg      90
              ||| |...|...|...| |...|...|...|...|...|...|
B_licheniform 43 atc---atttgcgaatggatc--gtcattgaagctgttgcccttgattgcg      87

SEQ175      91 ctgcgggtcaaccgtccgtttacaatcagcagggcgagcgggaaacgga      140
              .| |...|...|...|...|...| |...|...|...|
B_licheniform 88 at-----tctgattgtttgactgccgc---cgaat-ggagccgg-      123

SEQ175      141 ttttattcaatgtgtcgtttggcgccgcc---ggcgaaaacgtcgcc      186
              |||...|...| |...|...| |...|...| |...|...|
B_licheniform 124 -----ttcattttgtc-----cgccgccaaagtgttggcctccctggcc      162

SEQ175      187 aactttttgaaaaagggagcttggctgggtgtcgatggcgcactgca---      233
              ..|...|...|...|...|...|...|...|...|...|...|
B_licheniform 163 tccgctgtaaccgcgggaaccagaaccgcgcctttaggctccagaaatt      212

SEQ175      234 -aaccc--gcagctatgaaaatcaagaaggtcggcgtg-tgtacgtgacg      279
              |||. |...| |...|...|...|...|...| |...|...|
B_licheniform 213 gaacactttcagct-tgaacttcogtgacgtatacacgctgtccctgctg      261

SEQ175      280 gaagtgggtggc-----tgatagcgtccaatttcttgagccgaaagga      321
              ....|...| |...|...| |...|...| |...|...|
B_licheniform 262 attttcatagctgcgcgtttgcaaacgtcca---tctacaccgcgaag--      306

SEQ175      322 acgagc-----ga-----gcagcg---agg---ggcgacagcagg      350
              ||...| |...| |...| |...| |...|...|
B_licheniform 307 acttccttttttaaggaaatttgcaacgttttcggcttgccttctccaga      356

SEQ175      351 cggctactatgg--ggatcca--tcccattcg---ggcaagatcagaac      393
              |..| |...| |...| |...| |...| |...|...|
B_licheniform 357 caac-acagttgatgaaatcagcttcacgttcacccctgctgattcgtaaa      405
```



```
#####
# Program: needle
# Rundate: Mon Jul 31 07:21:22 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060731-07212194055950.output
#####

#=====
#
# Aligned_sequences: 2
# 1: SEQ175
# 2: B_halodurans
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 553
# Identity: 253/553 (45.8%)
# Similarity: 253/553 (45.8%)
# Gaps: 107/553 (19.3%)
# Score: 1074.0
#
#=====

SEQ175      1      atgattaaccg-cgtc----attttggtcggcaggttaacg--ag      38
              |||...|||. |||  |||.|||.|||.|||.|||. |
B_halodurans 1      ttagaatggcaaatcatcatcggaatatcgattggcttgccatcatttg      50

SEQ175      39      agatccggagttgcgttacactccaagcggagtg--ctgttgccac--      83
              ..|.|||.|||.|||.|||.|||.  |||.|||.  |.|||.|||
B_halodurans 51      caaacgggtcttctgagaaaccac---cggattgacgtccggagccacca      97

SEQ175      84      -gtttacgctcgcgggtca--accgtccgtttacaaatcagcagggcgagc      130
              .|||.|||.|||.|||.  |||.|||.  ...|...|  |||
B_halodurans 98      gattgttgcccgaatcattaccgcocatt---gggttggttaggg-gagc      143

SEQ175      131     gggaaacggattttattcaatgtgtcgtttggcgccgagggcggaaaac      180
              .|.|||.|||.|||.  |||.  |||.|||.|||.|||.  .....
B_halodurans 144     cgccaccaaagtt--gtcaa----cgtttgatcccccttggtttgtga      186

SEQ175      181     gtcgccaactttttgaaaaaggggagcttggtggtgtcgatggcgact      230
              |.|||.|||.|||.|||.  |||.|||.  |||.  |.|||.|||. ||
B_halodurans 187     gccgcgcggttcaaggaatt-gaacgctt-tctg---ccatgacc-tct      229

SEQ175      231     g---caaaccgcagctatgaaaatcaagaaggctg-----gcgtgtg      270
              |  |||.|||.|||.  |....|||.|||.  |||.|||.
B_halodurans 230     gtcacaaagactctgc---ggccttcattgtgtgcataactgcgcgtttg      276

SEQ175      271     tacgtgacggaagtgggtggtgatag-cgtccaatttcttgagccgaaaag      319
              .|||.|||.  |.|||.|||.|||.  |||.|||.  .....  |.|||.
B_halodurans 277     aatccgac--catcaacaccagctagacttccctttt-----tcaaata      318

SEQ175      320     gaacg-agcgagcagcgagggggcgacag-cagggcggtac---tatgggg      364
              [..]  ..|||.|||.  ..|||.|||.  |||.|||.  |||.  |.|||.
B_halodurans 319     gttcgccacgttctccgc-ttgcttccgccaaacgac-acagttaatgaa      366

SEQ175      365     atc-----cattcccatcgggcaagatc-agaaccaccaatatccga      406
              |||  |||.|||.  |||.|||.  |||.|||.  |||.  |.|||.
B_halodurans 367     atctgcttcgcgctctcctt---gttggttcgagaacggcggtttacag      413
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SEQ175           407 acgaaaaagggtttg----gccgcgatcg-atgacgatccttctgc--ca      448
                   .....|.|.|.| |   ||..|||.|||.|||. .|.|.| |.
B_halodurans     414 caagtgtaaaagtttgctacagcaaacacgctttggcggtg--tagcgcaact    461

SEQ175           449 atg---acg-gccagcgcgatcgatatattct--gatg--atgatttgcgc      489
                   ||   |||.|||.|||   ||   |||. |.|.|.|.|.|.
B_halodurans     462 ctggatcacgtgtgtaaccgcaccca-----ctaggacgcacgattttaaca    506

SEQ175           490 ttt       492
                   |
B_halodurans     507 t       507

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#####
# Program: needle
# Rundate: Mon Jul 31 07:22:20 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060731-07222012434590.output
#####

#=====
#
# Aligned_sequences: 2
# 1: SEQ175
# 2: B_clausii
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 552
# Identity: 257/552 (46.6%)
# Similarity: 257/552 (46.6%)
# Gaps: 126/552 (22.8%)
# Score: 1055.5
#
#=====

SEQ175      1      at-gattaaccgcgtc---attttggtcg-gcaggttaacgaga      39
              || ||..||..||| |||..||| ..|.....|
B_clausii   1 Ttaaaatggaagatcatcgctcggaatatcaatcgaaccgctattcgaga      50

SEQ175      40 gatccggagtttgcgtta-cactccaagcggagtggctgttgccacgttta      88
              .||| || ||||| ||...|...|..|||...||| |||
B_clausii   51 ---acgg-gt--cgttatcatatccattagaacggctgccacca-gttt-      92

SEQ175      89 cgctcgcggtc--aacgcgtcgtttacaaatcagcagggcgagcgg---g      133
              |..|| | ||||| |..|| | ||| |..||..|
B_clausii   93 -ggttgc---cagaacctt--ggttgc---cagc--gccgtactgatca      130

SEQ175     134 aaacggattttattcaatgtgtcgtttggcgccgccag--gcggaaaacg      181
              |||.....| |||||...| |..|||...|..| |||....
B_clausii  131 aaaccaggattattcccagag--gattggtttgactgttcgaggt---      175

SEQ175     182 tcgccaaactttttgaaaaaggaggcgtt--ggetggtgtcgatggccgac      229
              |||..||..| |..||| |..| ..|||..|||
B_clausii  176 tcgagaaatt-----ggacgctttcagc---aacgatttcgct-      210

SEQ175     230 tgcaaacccgcagct-----atgaaaatcaagaaggtcggcgtgtgtac      273
              |..|||..|||..| |..||| |..|..|||..|||
B_clausii  211 tacaaaaacgcgcctgccttcattattgtca--tagcttcgcgtttgcac      258

SEQ175     274 gtgacggaagt-ggtggtgatagcgtccaattttcttgagccgaaaggaa      322
              |||..| |...||..|..|..|||..|||..|...|..|
B_clausii  259 ---acggcgcgtcgactcctgcaaggctccctttttaaggaaattggcga      305

SEQ175     323 cgagcg-agc-----agcgaggggcgaca-----gcaggcggctact      358
              ||..| || |..||..|..|| |..||..|||
B_clausii  306 cgttctcagccggtttgcgccagacaacacagttaatgaagtcagcttct      355

SEQ175     359 atggggatccattcccatcgggcaagatcagaacc--accaatato--c      404
              |..||..|..| |..|..||..| |..||..|
B_clausii  356 -----cgttctcctt---gctggtttgaaaacggacggttgactgc      393

```

